

GenCore version 4.5									
34	462	34.4	543	1	CDP2_MOUSE	P49101	zea mays (m		
35	462	34.4	542	1	KCC1_MOUSE	P28552	mus musculu		
36	459	34.2	335	1	KCC1_SCPO	Q9P712	schizosachch		
37	458	34.1	512	1	KI10_ARATH	Q38997	arabidopsis		
38	457	34.0	542	1	KCC1_RAT	P08413	rattus norv		
39	457	34.0	664	1	KCCB_HUMAN	Q13554	homo sapien		
40	456.5	34.0	406	1	KPBH_RAT	P3125	rattus norv		
41	452.5	33.7	405	1	KPBH_HUMAN	P05318	oryctolagus		
42	452	33.7	386	1	KPBG_RABIT	Q62915	rattus norv		
43	450	33.5	909	1	CSKP_RAT	Q14536	homo sapien		
44	450	33.5	921	1	CSKP_HUMAN	Q70589	mus musculu		
45	450	33.5	924	1	CSKP_MOUSE				
ALIGNMENTS									
Searched:									
Scoring table: Biosum62									
Gapop 10.0 , Gapext 0.5									
Total number of hits satisfying chosen parameters: 105224									
Minimum DB seq length: 0									
Maximum DB seq length: 200000000									
Post-processing: Minimum Match 0%									
Maximum Match 100%									
Listing first 45 summaries									
Database : SwissProt_40.*									
Pred. No. 19 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.									
SUMMARIES									
Result	Score	Query	Length	DB	ID	Description			
No.		Match							
1	1124	83.7	1431	1	DARK_HUMAN	P53355 homo sapien	RESULT 1	STANDARD;	PRT; 1431 AA.
2	653.5	48.7	1176	1	KMIS_BOVIN	P28824 bos taurus	DAK_HUMAN	STANDARD;	PRT; 1431 AA.
3	647.5	48.2	1905	1	KMIS_CHICK	P11799 gallus gallus	STANDARD;	STANDARD;	PRT; 1431 AA.
4	642.9	47.8	1914	1	KMIS_HUMAN	Q15746 homo sapien	STANDARD;	STANDARD;	PRT; 1431 AA.
5	639.6	39.6	1912	1	KMIS_MOUSE	Q9gm70 oryctolagus cuniculus	STANDARD;	STANDARD;	PRT; 1431 AA.
6	638.0	47.5	414	1	K17A_HUMAN	Q8ee55 homo sapien	STANDARD;	STANDARD;	PRT; 1431 AA.
7	636.5	47.4	1147	1	KMIS_RABBIT	P28294 oryctolagus cuniculus	STANDARD;	STANDARD;	PRT; 1431 AA.
8	625.5	37.2	474	1	K17B_HUMAN	Q94768 homo sapien	STANDARD;	STANDARD;	PRT; 1431 AA.
9	611.5	45.5	438	1	KMIS_SHEEP	Q02827 ovis aries	STANDARD;	STANDARD;	PRT; 1431 AA.
10	571.5	42.6	607	1	KMPC_RABBIT	P07313 oryctolagus cuniculus	STANDARD;	STANDARD;	PRT; 1431 AA.
11	570.5	42.5	609	1	KMPC_RAT	P20689 rattus norvegicus	STANDARD;	STANDARD;	PRT; 1431 AA.
12	530.5	39.5	295	1	KMPC_DICDI	P25323 dictyostelia thermophila	STANDARD;	STANDARD;	PRT; 1431 AA.
13	509	37.9	473	1	KCC4_HUMAN	Q16566 homo sapien	STANDARD;	STANDARD;	PRT; 1431 AA.
14	506	37.7	474	1	KCC4_RAT	P13234 rattus norvegicus	STANDARD;	STANDARD;	PRT; 1431 AA.
15	505	37.6	469	1	KCC4_MOUSE	P08414 mus musculus	STANDARD;	STANDARD;	PRT; 1431 AA.
16	500	37.2	3038	1	KTCO_HUMAN	Q15962 homo sapien	STANDARD;	STANDARD;	PRT; 1431 AA.
17	495	36.9	533	1	KCCD_RAT	P15791 rattus norvegicus	STANDARD;	STANDARD;	PRT; 1431 AA.
18	488	36.3	499	1	KCCD_HUMAN	Q13557 homo sapien	STANDARD;	STANDARD;	PRT; 1431 AA.
19	485	36.1	370	1	KCC1_HUMAN	Q14012 homo sapien	STANDARD;	STANDARD;	PRT; 1431 AA.
20	485	36.1	374	1	KCC1_RAT	Q63450 rattus norvegicus	STANDARD;	STANDARD;	PRT; 1431 AA.
21	483.5	36.0	424	1	KPSH_HUMAN	P11801 homo sapien	STANDARD;	STANDARD;	PRT; 1431 AA.
22	483	36.0	542	1	CDP3_ORYSEA	P55684 oryza sativa	STANDARD;	STANDARD;	PRT; 1431 AA.
23	480	35.7	533	1	CDPK1_HUMAN	P55683 oryza sativa	STANDARD;	STANDARD;	PRT; 1431 AA.
24	479.5	35.7	740	1	CDKL_HUMAN	P11730 rattus norvegicus	STANDARD;	STANDARD;	PRT; 1431 AA.
25	478.5	35.6	433	1	CDKL_RAT	Q008875 rattus norvegicus	STANDARD;	STANDARD;	PRT; 1431 AA.
26	478.5	35.6	478	1	CDKL_MOUSE	Q911m8 mus musculus	STANDARD;	STANDARD;	PRT; 1431 AA.
27	475	35.4	478	1	KCCA_RAT	P11275 rattus norvegicus	STANDARD;	STANDARD;	PRT; 1431 AA.
28	471	35.1	478	1	KCCA_MOUSE	P11798 mus musculus	STANDARD;	STANDARD;	PRT; 1431 AA.
29	469	34.9	527	1	KCCG_RAT	P11730 rattus norvegicus	STANDARD;	STANDARD;	PRT; 1431 AA.
30	468	34.8	532	1	CDPK_DAICA	P28582 daucus carota	STANDARD;	STANDARD;	PRT; 1431 AA.
31	468	34.8	610	1	CDPL_ARATH	Q08850 arabidopsis thaliana	STANDARD;	STANDARD;	PRT; 1431 AA.
32	464	34.5	534	1	CDPL_ORYSA	P53682 oryza sativa	STANDARD;	STANDARD;	PRT; 1431 AA.
33	462	34.4	508	1	CDPR_SOYBN	P28583 glycine max	STANDARD;	STANDARD;	PRT; 1431 AA.

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DR	PROSITE; PS00107; PROTEIN KINASE ATP; 1.	RL	J. Biochem. 112:786-791(1992).
DR	PROSITE; PS0011; PROTEIN KINASE DOM; 1.	CC	-I- FUNCTION: CALCIUM/CALMODULIN-DEPENDENT ENZYME RESPONSIBLE FOR SMOOTH MUSCLE CONTRACTION VIA PHOSPHORYLATION OF A SPECIFIC SERINE
KW	transferase; Serine/threonine-protein kinase; Calmodulin-binding; phosphorylation; ATP-binding; Repeat; ANK repeat; Apoptosis.	CC	IN THE N-TERMINUS OF MYOSIN LIGHT CHAINS (MLC), AN EVENT THAT FACILITATES MYOSIN INTERACTION WITH ACTIN FILAMENTS.
FT	DOMAIN 13 266 PROTEIN KINASE.	CC	-I- CATALYTIC ACTIVITY: ATP + [myosin light-chain] = ADP + [myosin
FT	DOMAIN 267 334 CALMODULIN-BINDING.	CC	light-chain] phosphate.
FT	REPEAT 378 407 ANK 1.	CC	-I- SUBUNIT: TELOKIN Binds CALMODULIN.
FT	REPEAT 411 440 ANK 2.	CC	-I- ALTERNATIVE PRODUCTS: AT LEAST 3 ISOFORMS OF MLCK ARE PRODUCED BY ALTERNATIVE INITIATION, A NON-MUSCLE FORM (WHICH IS THE LONGEST FORM); A SMOOTH-MUSCLE FORM AND TELOKIN (A C-TERMINAL SECTION WITH NO CATALYTIC ACTIVITY).
FT	REPEAT 444 473 ANK 3.	CC	-I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
FT	REPEAT 478 507 ANK 4.	CC	-I- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
FT	REPEAT 511 540 ANK 5.	CC	-I- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
FT	REPEAT 544 573 ANK 6.	CC	-I- SIMILARITY: BY SIMILARITY.
FT	REPEAT 577 605 ANK 7.	CC	-I- SIMILARITY: BY SIMILARITY.
FT	REPEAT 610 639 ANK 8.	CC	-I- SIMILARITY: BY SIMILARITY.
FT	REPEAT 876 905 ANK 9.	CC	-I- SIMILARITY: BY SIMILARITY.
FT	REPEAT 1163 1197 ANK 10.	CC	-I- SIMILARITY: DEATH.
FT	NP_BIND 19 27 ATP (BY SIMILARITY).	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).
FT	BINDING 42 42 ATP (BY SIMILARITY).	CC	or send an email to license@isb-sib.ch).
ACT_SITE	139 139 MUTAGEN 42 42 SEQUENCE 1431 AA; 160017 MW; 9E884811004A155B CRC64;	CC	CC
Query Match	83.7%; Score 1124; DB 1; Length 1431;	CC	CC
Best Local Similarity	79.5%; Pred. No. 5. 8e-65;	DR	EMBL; S57131; AAB25794; 1; -.
Matches	209; Conservative 41; Mismatches 13; Indels 0; Gaps 0;	DR	HSSP; P56276; ITAK.
Ov	1 YD1GEELGGQPAVKKCREKSTGLEYAKIKKKROSRSRGSRSRGSVSETEREVSIQLRQL 60	DR	InterPro; IPR000719; Euk_Pkinase.
Db	13 YD1GEELGGQPAVKKCREKSTGLEYAKIKKKROSRSRGSRSRGSVSETEREVSIQLRQL 72	DR	InterPro; IPR03961; FN_ITI.
Ov	61 HNIVITLHDVYBVRNTDVTILELLVSGELFLRAQESLSBEATSFKIQIDGYNYLT 120	DR	InterPro; IPR000006; Ig_MHC.
Db	73 HNIVITLHDVYBVRNTDVTILELLVSGELFLRAQESLSBEATSFKIQIDGYNYLT 132	DR	InterPro; IPR00598; Ig_C2.
Ov	121 KRIAHDLKPENIMLKDKNIPPIPHKLIDFLGIAHELEDGYVEEKFGTPPEVAPENVYE 180	DR	InterPro; IPR003600; Ig_Like.
Db	133 LQIAHDFDLKPENIMLKDNRVPRPKITIDFLGIAHKIDFGNEFKFNGTFPEVAPENVYE 192	DR	InterPro; IPR002290; Ser_thr_Pkinase.
Ov	181 PGLEADMSWSGVVITYLLSGASPLFGDTKQETLANITSYSDFDEFFSITSELAKDFI 240	DR	Pfam; PF00041; fn3; 1.
Db	193 PGLEADMSWSGVVITYLLSGASPLFGDTKQETLANAVSVVYEFDEYFSNTSALAKDFI 252	DR	Pfam; PF00069; Pkinase; 1.
Ov	241 RKLVLVETRKRLQTQALRHPW 263	DR	SMART; SM00410; Ig_Like; 1.
Db	253 RRLVVKDKKKRTIQDSLQHPW 275	DR	SMART; SM00408; IgC2; 2.
RESURT	2	DR	SMART; SM00220; S_TKC; 1.
ID	KMLS_BOVIN STANDARD; PRT; 1176 AA.	DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
AC	Q28824; 028824; 15-JUL-1998 (Rel. 36, Created)	DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DT	15-JUL-1998 (Rel. 36, Last sequence update)	DR	PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DE	Myosin light chain kinase, smooth muscle (EC 2.7.1.117) (MLCK) [Contains: Telokin].	KW	Transferase; Serine/threonine-protein kinase; Calmodulin-binding; ATP-binding; Phosphorylation; Immunoglobulin domain; Repeat; Alternative initiation.
GN	MYLK.	FT	CHAIN 1 1176 MYOSIN LIGHT CHAIN KINASE, SMOOTH-MUSCLE
OS	Bos taurus (Bovine).	FT	INIT_MET 1022 1022 1176 FOR TELOKIN.
OC	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bivalvia; Bivalvia; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.	FT	DOMAIN 100 291 16 X 12 AA TANDEM REPEATS.
NCBI	TAXID 9913;	FT	REPEAT 100 111 1.
RN	[1] SEQUENCE FROM N.A.	FT	REPEAT 112 123 2.
RR	SEQUENCE FROM N.A.	FT	REPEAT 124 135 3 (INCOMPLETE).
RC	TISSUE=Stomach;	FT	REPEAT 136 147 4.
RX	MEDLINE=9230118; PubMed=1284247;	FT	REPEAT 148 159 5.
RA	Kobayashi H., Inoue A., Mikawa T., Kuwayama H., Hotta Y., Masaki T., Ebashi S.; "Isolation of cDNA for bovine stomach 155 kDa protein exhibiting myosin light chain kinase activity";	FT	REPEAT 160 171 6.
RT	"Isolation of cDNA for bovine stomach 155 kDa protein exhibiting myosin light chain kinase activity";	FT	REPEAT 172 183 7.
RT	"Isolation of cDNA for bovine stomach 155 kDa protein exhibiting myosin light chain kinase activity";	FT	REPEAT 184 195 8.
RT	"Isolation of cDNA for bovine stomach 155 kDa protein exhibiting myosin light chain kinase activity";	FT	REPEAT 196 207 9.
RT	"Isolation of cDNA for bovine stomach 155 kDa protein exhibiting myosin light chain kinase activity";	FT	REPEAT 208 219 10.
FT	REPEAT 220 231 11.	FT	REPEAT 220 231 11.
FT	REPEAT 232 243 12.	FT	REPEAT 232 243 12.
FT	REPEAT 244 255 13.	FT	REPEAT 244 255 13.
FT	REPEAT 256 267 14.	FT	REPEAT 256 267 14.
FT	REPEAT 268 279 15.	FT	REPEAT 268 279 15.
FT	REPEAT 280 291 16.	FT	REPEAT 280 291 16.
FT	DOMAIN 603 673 FIBRONECTIN_TYPE-III.	FT	DOMAIN 603 673 FIBRONECTIN_TYPE-III.
FT	DOMAIN 675 980 PROTEIN_KINASE.	FT	DOMAIN 675 980 PROTEIN_KINASE.
FT	DOMAIN 972 1035 CALMODULIN-BINDING.	FT	DOMAIN 972 1035 CALMODULIN-BINDING.
FT	DOMAIN 1084 1151 IG-LIKE_C2-TYPE DOMAIN.	FT	DOMAIN 1084 1151 IG-LIKE_C2-TYPE DOMAIN.
FT	NP_BIND 731 739 ATP (BY SIMILARITY).	FT	NP_BIND 731 739 ATP (BY SIMILARITY).
FT	BINDING 754 754 ATP (BY SIMILARITY).	FT	BINDING 754 754 ATP (BY SIMILARITY).
ACT_SITE	846 846	FT	ACT_SITE 846 846

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